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<input type="checkbox"/>	L8	dsm with 11988	6
<input type="checkbox"/>	L7	dsm with 11980	1
		<i>DB=PGPB; PLUR=YES; OP=ADJ</i>	
<input type="checkbox"/>	L6	alkaline sphingomyelinase	2
		<i>DB=EPAB,JPAB; PLUR=YES; OP=ADJ</i>	
<input type="checkbox"/>	L5	alkaline sphingomyelinase	1
		<i>DB=USOC; PLUR=YES; OP=ADJ</i>	
<input type="checkbox"/>	L4	alkaline sphingomyelinase	0
		<i>DB=DWPI; PLUR=YES; OP=ADJ</i>	
<input type="checkbox"/>	L3	alkaline sphingomyelinase	3
		<i>DB=USPT; PLUR=YES; OP=ADJ</i>	
<input type="checkbox"/>	L2	alkaline sphingomyelinase	0
<input type="checkbox"/>	L1	6562336.pn.	1

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NiceProt

View of

TrEMBL:

Q8IUS8

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Entry information

Entry name	Q8IUS8
Primary accession number	Q8IUS8
Secondary accession numbers	None
Entered in TrEMBL in	Release 23, March 2003
Sequence was last modified in	Release 24, June 2003
Annotations were last modified in	Release 25, October 2003

Name and origin of the protein

★ Protein name	Hypothetical protein
★ Synonym	Intestinal alkaline sphingomyelinase
Gene name	None
From	<u>Homo sapiens (Human)</u> [TaxID: 9606]
Taxonomy	<u>Eukaryota</u> ; <u>Metazoa</u> ; <u>Chordata</u> ; <u>Craniata</u> ; <u>Vertebrata</u> ; <u>Euteleostomi</u> ; <u>Mammalia</u> ; <u>Eutheria</u> ; <u>Primates</u> ; <u>Catarrhini</u> ; <u>Hominidae</u> ; <u>Homo</u> .

References

[1] SEQUENCE FROM NUCLEIC ACID.**TISSUE=Colon;**

MEDLINE=22388257; PubMed=12477932; [NCBI, ExPASy, EBI, Israel, Japan]

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2] SEQUENCE FROM NUCLEIC ACID.**TISSUE=Colon;****Strausberg R.;**

Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.

[3] SEQUENCE FROM NUCLEIC ACID.

Duan R.-D., Bergman T., Xu N., Wu J., Cheng Y., Duan J., Nelander S., Palmberg C., Nilsson A.;

"Identification of human intestinal alkaline sphingomyelinase as a novel ecto-enzyme related to the nucleotide phosphodiesterase family.";

J. Biol. Chem. 0:0-0(2003).

Comments

None

Cross-references

EMBL	BC041453; AAH41453.2; -. [EMBL / GenBank / DDBJ] [CoDingSequence] AY230663; AAP69661.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]	
GO	GO:0016787; Molecular function: hydrolase activity (<i>inferred from electronic annotation</i>). GO:0009117; Biological process: nucleotide metabolism (<i>inferred from electronic annotation</i>).	
Ensembl	Q8IUS8; Homo sapiens. [Entry / Contig view]	
InterPro	IPR002591; Phosphodiect. Graphical view of domain structure.	
Pfam	PF01663; Phosphodiect; 1. Pfam graphical view of domain structure.	
ProDom	[Domain structure / List of seq. sharing at least 1 domain]	
HOVERGEN	[Family / Alignment / Tree]	
ProtoMap	Q8IUS8.	
PRESAGE	Q8IUS8.	
ModBase	Q8IUS8.	
SMR	Q8IUS8; A40560D61140F692.	
SWISS-2DPAGE	Get region on 2D PAGE.	
UniRef	View cluster of proteins with at least <u>50%</u> / <u>90%</u> identity.	
Keywords		
<u>Hypothetical protein.</u>		
Features		
None		
Sequence information		
Length: 458 AA Da	Molecular weight: 51477	CRC64: A40560D61140F692 [This is a checksum on the sequence]

10	20	30	40	50	60
MRGPAVLLTV	ALATLLAPGA	GAPVQSQGSQ	NKLLLVSFDG	FRWNYDQDVD	TPNLDAMARD
70	80	90	100	110	120
GVKARYMTPA	FVTMTSPCHF	TLVTGKYIEN	HGVVHNMYYN	TTSKVKLPYH	ATLGIQRWWD
130	140	150	160	170	180
NGSVPIWITA	QRQGLRAGSF	FYPGGNVTYQ	GVAVTRSRKE	GIAHNYKNET	EWRANIDTVM
190	200	210	220	230	240
AWFTEEDLDL	VTLYFGEPDS	TGHRYGPESP	ERREMRVQVD	RTVGYLRESI	ARNHLTDRLN
250	260	270	280	290	300
LIITSDHGMT	TVDKRAGDLV	EFHKFPNFTF	RDIEFELLDY	GPNGMLLPKE	GRLEKVYDAL
310	320	330	340	350	360
KDAHPKLHVV	KKEAFPEAFH	YANNPRVTPL	LMYSDLGYVI	HGRINVQFNN	GEHGFDNKDM
370	380	390	400	410	420
DMKTIFRAVG	PSFRAGLEVE	PFESVHVYEL	MCRLLGIVPE	ANDGHLATLL	PMLHTESALP
430	440	450			
PDGRPTLLPK	GRSALPPSSR	PLLVMGLLGT	VILLSEVA		

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NiceZyme View of ENZYME: EC 3.1.4.12

Official Name	
Sphingomyelin phosphodiesterase.	
Alternative Name(s)	
Acid sphingomyelinase. Neutral sphingomyelinase.	
Reaction catalysed	
$ \begin{array}{l} \text{Sphingomyelin} \\ + \text{H(2)O} \\ \hline \text{N-acylsphingosine} \\ + \text{choline phosphate} \end{array} $	
Comments	
<ul style="list-style-type: none"> Has very little activity on phosphatidylcholine. 	
Human Genetic Disease(s)	
Niemann-Pick disease, type A	MIM:257200
Niemann-Pick disease, type B	MIM:607616
Cross-references	
Biochemical Pathways; map number(s)	C8
BRENDA	3.1.4.12
EMP/PUMA	3.1.4.12
WIT	3.1.4.12
Kyoto University LIGAND chemical database	3.1.4.12
IUBMB Enzyme Nomenclature	3.1.4.12
IntEnz	3.1.4.12
MEDLINE	Find literature relating to 3.1.4.12
Swiss-Prot	Q10916 , ASM1_CAEEL ; Q23498 , ASM2_CAEEL ; Q9UAY4 , ASM3_CAEEL ; P17405 , ASM_HUMAN ; Q04519 , ASM_MOUSE ; O45870 , NSMA_CAEEL ; Q9VZS6 , NSMA_DROME ; O60906 , NSMA_HUMAN ; O70572 , NSMA_MOUSE ; Q9ET64 , NSMA_RAT ; O74369 , NSMA_SCHPO ; P09599 , PHL1_BACCE ; P59115 , PHL1_LEPIN ; P11889 , PHL2_BACCE ; P59116 , PHL2_LEPIN ;